P4/10

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/510,408

CRF Edit Date: 10/19/04

Edited by: AZ

_____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

_____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

_____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

_/__ Deleted: _/_ invalid beginning/end-of-file text ; ___ page numbers

_____ Inserted mandatory headings/numeric identifiers, specifically:

_____

_____ Moved responses to same line as heading/numeric identifier, specifically:

_____

_____ Other:

_____
_____
_____

Revised 09/09/2003

PCT

RAW SEQUENCE LISTING   DATE: 10/19/2004
PATENT APPLICATION: US/10/510,408   TIME: 14:41:00

        Input Set : N:\AMC\PTO.AMC.txt
        Output Set: N:\CRF4\10192004\J510408.raw

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   3 <110> APPLICANT: Jorgensen, Steen Troels
   4         Olsen, Peter Bjarke
   5         Andersen, Jens Tonne
   6         Rasmussen, Michael Dolberg
   8 <120> TITLE OF INVENTION: Improved Bacillus Host Cell
  10 <130> FILE REFERENCE: 10295.204-US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/510,408
C--> 12 <141> CURRENT FILING DATE: 2004-10-05
  12 <160> NUMBER OF SEQ ID NOS: 191
  14 <170> SOFTWARE: PatentIn version 3.3
  16 <210> SEQ ID NO: 1
  17 <211> LENGTH: 1055
  18 <212> TYPE: DNA
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  24 <222> LOCATION: (34)..(552)
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  31 aaa atc ggt tta ttg ctt att gga agt ctg ctg gcc gcg ctc agc ttt       102
  32 Lys Ile Gly Leu Leu Leu Ile Gly Ser Leu Leu Ala Ala Leu Ser Phe
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  35 cac ctg gag gcc ttg gcc gaa aag ccg gct aaa gtt caa atc cag ctt       150
  36 His Leu Glu Ala Leu Ala Glu Lys Pro Ala Lys Val Gln Ile Gln Leu
  37      25                  30                  35
  39 gaa aag gtt tat ctg gac gga gac gtt gga att gag aat aaa gta gag       198
  40 Glu Lys Val Tyr Leu Asp Gly Asp Val Gly Ile Glu Asn Lys Val Glu
  41 40                  45                  50                  55
  43 gcc gct cgc aca ctg gaa gac ttt aaa gct gct tat aaa ggg tgg cag       246
  44 Ala Ala Arg Thr Leu Glu Asp Phe Lys Ala Ala Tyr Lys Gly Trp Gln
  45              60                  65                  70
  47 ctc atc gat cag aaa aag ggg ttt att ctg ttt cgc aaa cag gtg gac       294
  48 Leu Ile Asp Gln Lys Lys Gly Phe Ile Leu Phe Arg Lys Gln Val Asp
  49              75                  80                  85
  51 gac att tct ccc ctc agc aaa aca aac ggt tat atc gga gtg act gaa       342
  52 Asp Ile Ser Pro Leu Ser Lys Thr Asn Gly Tyr Ile Gly Val Thr Glu
  53          90                  95                  100
  55 gat ggc gtg att tcg act ttt cac ggt cgc ccg ggc atc tta tca gaa       390
  56 Asp Gly Val Ile Ser Thr Phe His Gly Arg Pro Gly Ile Leu Ser Glu
  57      105                 110                 115
  59 ccc att caa tcg ttt ttt cag att gat ata aag cgg ctg gaa agc cgg       438
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60 Pro Ile Gln Ser Phe Phe Gln Ile Asp Ile Lys Arg Leu Glu Ser Arg
61 120                 125                 130                 135
63 atg gcg gat gat ctg cgc aaa ggg ata cca tac cgc acg aaa aag gaa        486
64 Met Ala Asp Asp Leu Arg Lys Gly Ile Pro Tyr Arg Thr Lys Lys Glu
65                 140                 145                 150
67 ttt gaa cat gtc att gaa gcc gta aaa tca tcc gga agc caa cat cat        534
68 Phe Glu His Val Ile Glu Ala Val Lys Ser Ser Gly Ser Gln His His
69                 155                 160                 165
71 gta gaa gat atg aag aca tgacgctgtt atgtcttttt tcagctgcag              582
72 Val Glu Asp Met Lys Thr
73           170
75 acagaagctt ttttagcgaa catatgttaa ctttttcatt ctagctttgc ctgttttgtg     642
77 ttacaatgaa gagcagtcaa agaggtgaat gaacgttgat cgaattcgta aaagggacga     702
79 ttgattatgt atcgccccaa tatattgtca ttgaaaacgg cgggatcggc tatcagatct     762
81 tcacgccaaa tccgtttatt tataagaaaa acagcaaaga aacaatctat acataccatt     822
83 atgtaagaga agacacgaat gcgctgtacg gcttttcgac aagggaagaa aaaatgctgt     882
85 ttacgaaaat gctgaatgtt acggggatcg gcccaaaagg agcgcttgcg atcctcgctt    ·942
87 ccggcgatcc gggagcggtg attgaagcga tcgagaatga ggacgaagca tttctcgtca    1002
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93 <211> LENGTH: 173
94 <212> TYPE: PRT
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104                 20                 25                 30
107 Ala Lys Val Gln Ile Gln Leu Glu Lys Val Tyr Leu Asp Gly Asp Val
108                 35                 40                 45
111 Gly Ile Glu Asn Lys Val Glu Ala Ala Arg Thr Leu Glu Asp Phe Lys
112       50                 55                 60
115 Ala Ala Tyr Lys Gly Trp Gln Leu Ile Asp Gln Lys Lys Gly Phe Ile
116 65                 70                 75                 80
119 Leu Phe Arg Lys Gln Val Asp Asp Ile Ser Pro Leu Ser Lys Thr Asn
120                 85                 90                 95
123 Gly Tyr Ile Gly Val Thr Glu Asp Gly Val Ile Ser Thr Phe His Gly
124                 100                 105                 110
127 Arg Pro Gly Ile Leu Ser Glu Pro Ile Gln Ser Phe Phe Gln Ile Asp
128                 115                 120                 125
131 Ile Lys Arg Leu Glu Ser Arg Met Ala Asp Asp Leu Arg Lys Gly Ile
132       130                 135                 140
135 Pro Tyr Arg Thr Lys Lys Glu Phe Glu His Val Ile Glu Ala Val Lys
136 145                 150                 155                 160
139 Ser Ser Gly Ser Gln His His Val Glu Asp Met Lys Thr
140                 165                 170
143 <210> SEQ ID NO: 3
144 <211> LENGTH: 2130
145 <212> TYPE: DNA
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RAW SEQUENCE LISTING   DATE: 10/19/2004
PATENT APPLICATION: **US/10/510,408**   TIME: 14:41:00

Input Set : **N:\AMC\PTO.AMC.txt**
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149 <220> FEATURE:
150 <221> NAME/KEY: CDS
151 <222> LOCATION: (501)..(2039)
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158 cgaaaatgaa cgttttcagc caatccggcg tcggtgtatg gcccaatacg accaatataa   180
160 ttcccacgcc tttcgaaaca tcaatccact ctattctttt ctgcaacacg ggtatctcct   240
162 ttcagaccgc ttcgccccat aagaaagggt ttacacataa tgtaccatca tccccgcctt   300
164 tcttcctccg cgaatcacgc ctcaaggcga tttttaatcg tcaggaaata ttttgttcat   360
166 cttcttgtaa tgatcgattc tatttttaa catactcagc acatactgcg tttcttattc   420
168 tcatcatgag gaaccagacc atgcaacccg tcttataatg taatgatctt ttcatcagaa   480
170 caaaagagga caggtgaaac atg aaa ctt gaa aaa ttc gtt gac cgg ctc ccc   533
171   Met Lys Leu Glu Lys Phe Val Asp Arg Leu Pro
172   1   5   10
174 att ccg caa gtg ctt caa ccc caa agc aaa agc aag gaa atg acc tat   581
175 Ile Pro Gln Val Leu Gln Pro Gln Ser Lys Ser Lys Glu Met Thr Tyr
176   15   20   25
178 tat gaa gtc acc atg aaa gaa ttt cag cag cag ctt cac cgc gat ctg   629
179 Tyr Glu Val Thr Met Lys Glu Phe Gln Gln Gln Leu His Arg Asp Leu
180   30   35   40
182 ccg ccg act cgg ctg ttt gga tat aac gga gtt tat ccc ggc cct acc   677
183 Pro Pro Thr Arg Leu Phe Gly Tyr Asn Gly Val Tyr Pro Gly Pro Thr
184   45   50   55
186 ttc gaa gtg cag aaa cac gaa aaa gtc gca gtc aag tgg tta aat aag   725
187 Phe Glu Val Gln Lys His Glu Lys Val Ala Val Lys Trp Leu Asn Lys
188 60   65   70   75
190 ctt ccg gat cgc cat ttt ctc ccc gtc gac cat acg ctt cac gat gac   773
191 Leu Pro Asp Arg His Phe Leu Pro Val Asp His Thr Leu His Asp Asp
192   80   85   90
194 ggc cat cac gaa cat gaa gtg aag acg gtc gtt cat ttg cac gga ggc   821
195 Gly His His Glu His Glu Val Lys Thr Val Val His Leu His Gly Gly
196   95   100   105
198 tgt acg cct gct gac agc gac gga tat cct gag gct tgg tac aca aaa   869
199 Cys Thr Pro Ala Asp Ser Asp Gly Tyr Pro Glu Ala Trp Tyr Thr Lys
200   110   115   120
202 gac ttc cat gca aaa ggc cct ttc ttt gaa agg gag gtg tat gaa tat   917
203 Asp Phe His Ala Lys Gly Pro Phe Phe Glu Arg Glu Val Tyr Glu Tyr
204   125   130   135
206 ccg aat gag cag gat gct aca gct ctt tgg tat cat gac cat gca atg   965
207 Pro Asn Glu Gln Asp Ala Thr Ala Leu Trp Tyr His Asp His Ala Met
208 140   145   150   155
210 gcc atc aca agg ctg aat gta tat gcg ggg ctt gtc ggt tta tat ttt   1013
211 Ala Ile Thr Arg Leu Asn Val Tyr Ala Gly Leu Val Gly Leu Tyr Phe
212   160   165   170
214 att cgc gac agg gaa gag cgt tca ttg aac ttg ccg aag gga gaa tat   1061
215 Ile Arg Asp Arg Glu Glu Arg Ser Leu Asn Leu Pro Lys Gly Glu Tyr
216   175   180   185

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218 gaa atc ccg ctt ttg att cag gat aaa tca ttt cat gaa gat ggt tca    1109
219 Glu Ile Pro Leu Leu Ile Gln Asp Lys Ser Phe His Glu Asp Gly Ser
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222 ttg ttt tat ccg cgg cag cct gac aac cct tcg ccg gat ctt ccg gac    1157
223 Leu Phe Tyr Pro Arg Gln Pro Asp Asn Pro Ser Pro Asp Leu Pro Asp
224     205                 210                 215
226 ccg tcg att gtt ccg gct ttt tgc ggt gat acc att tta gtc aac ggc    1205
227 Pro Ser Ile Val Pro Ala Phe Cys Gly Asp Thr Ile Leu Val Asn Gly
228 220                 225                 230                 235
230 aag gta tgg cct ttc gct gaa ctg gaa ccc cga aaa tac cgt ttt cgg    1253
231 Lys Val Trp Pro Phe Ala Glu Leu Glu Pro Arg Lys Tyr Arg Phe Arg
232     .               240                 245                 250
234 ata ctg aac gcc tcc aat acg aga atc ttt gag ctg tat ttc gat cat    1301
235 Ile Leu Asn Ala Ser Asn Thr Arg Ile Phe Glu Leu Tyr Phe Asp His
236             255                 260                 265
238 gac atc aca tgt cat caa atc ggc acg gac ggc ggt ctt ctg cag cat    1349
239 Asp Ile Thr Cys His Gln Ile Gly Thr Asp Gly Gly Leu Leu Gln His
240         270                 275                 280
242 ccg gtc aaa gtc aat gaa ctg gtg atc gcg ccg gct gaa agg tgc gat    1397
243 Pro Val Lys Val Asn Glu Leu Val Ile Ala Pro Ala Glu Arg Cys Asp
244     285                 290                 295
246 atc atc gtt gat ttt tca cga gca gaa gga aaa acc gtg aca ctg aaa    1445
247 Ile Ile Val Asp Phe Ser Arg Ala Glu Gly Lys Thr Val Thr Leu Lys
248 300                 305                 310                 315
250 aaa cgg atc ggc tgc ggc gga caa gac gca gat ccc gat act gat gcc    1493
251 Lys Arg Ile Gly Cys Gly Gly Gln Asp Ala Asp Pro Asp Thr Asp Ala
252             320                 325                 330
254 gac atc atg caa ttc cgc atc tca aaa cct ttg aag caa aaa gat aca    1541
255 Asp Ile Met Gln Phe Arg Ile Ser Lys Pro Leu Lys Gln Lys Asp Thr
256             335                 340                 345
258 agt tca ttg ccg aga ata ttg aga aag cgc cca ttt tac cgg aga cac    1589
259 Ser Ser Leu Pro Arg Ile Leu Arg Lys Arg Pro Phe Tyr Arg Arg His
260         350                 355                 360
262 aag atc aat gcc ctc aga aat ctg tca ttg ggc gcg gcc gtt gac caa    1637
263 Lys Ile Asn Ala Leu Arg Asn Leu Ser Leu Gly Ala Ala Val Asp Gln
264     365                 370                 375
266 tat gga aga cct gtt ctg ctt tta aac aac aca aag tgg cat gaa ccg    1685
267 Tyr Gly Arg Pro Val Leu Leu Leu Asn Asn Thr Lys Trp His Glu Pro
268 380                 385                 390                 395
270 gta acc gaa aca ccc gca ctc ggc agc act gag atc tgg tcg atc atc    1733
271 Val Thr Glu Thr Pro Ala Leu Gly Ser Thr Glu Ile Trp Ser Ile Ile
272                 400                 405                 410
274 aat gcc gga agg gcg atc cat ccg atc cat tta cat ctt gtt caa ttt    1781
275 Asn Ala Gly Arg Ala Ile His Pro Ile His Leu His Leu Val Gln Phe
276             415                 420                 425
278 atg att ctc gac cac cgg ccg ttt gat atc gag cgg tat cag gaa aac    1829
279 Met Ile Leu Asp His Arg Pro Phe Asp Ile Glu Arg Tyr Gln Glu Asn
280         430                 435                 440
282 gga gaa ctt gtt ttt acc ggt ccg gca gtt cct ccg gca ccg aat gaa    1877
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283 Gly Glu Leu Val Phe Thr Gly Pro Ala Val Pro Pro Ala Pro Asn Glu
284     445             450             455
286 aag ggg ctg aaa gac acc gtc aaa gta ccc ccg ggt tca gtg acg cgc    1925
287 Lys Gly Leu Lys Asp Thr Val Lys Val Pro Pro Gly Ser Val Thr Arg
288 460             465             470             475
290 att atc gcc acc ttt gcg ccg tac agc ggc aga tat gtt tgg cac tgc    1973
291 Ile Ile Ala Thr Phe Ala Pro Tyr Ser Gly Arg Tyr Val Trp His Cys
292             480             485             490
294 cac atc ctt gag cac gaa gat tac gat atg atg cgc cct ctt gaa gtg    2021
295 His Ile Leu Glu His Glu Asp Tyr Asp Met Met Arg Pro Leu Glu Val
296             495             500             505
298 aca gat gtt cgt cat caa taagaaaag cctccgcatt tggaggcttt           2069
299 Thr Asp Val Arg His Gln
300         510         ,
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319             20              25              30
322 Lys Glu Phe Gln Gln Gln Leu His Arg Asp Leu Pro Pro Thr Arg Leu
323         35      ,       40              45
326 Phe Gly Tyr Asn Gly Val Tyr Pro Gly Pro Thr Phe Glu Val Gln Lys
327     50              55              60
330 His Glu Lys Val Ala Val Lys Trp Leu Asn Lys Leu Pro Asp Arg His
331 65              70              75              80
334 Phe Leu Pro Val Asp His Thr Leu His Asp Asp Gly His His Glu His
335             85              90              95
338 Glu Val Lys Thr Val Val His Leu His Gly Gly Cys Thr Pro Ala Asp
339             100             105             110
342 Ser Asp Gly Tyr Pro Glu Ala Trp Tyr Thr Lys Asp Phe His Ala Lys
343         115             120             125
346 Gly Pro Phe Phe Glu Arg Glu Val Tyr Glu Tyr Pro Asn Glu Gln Asp
347     130             135             140
350 Ala Thr Ala Leu Trp Tyr His Asp His Ala Met Ala Ile Thr Arg Leu
351 145             150             155             160
354 Asn Val Tyr Ala Gly Leu Val Gly Leu Tyr Phe Ile Arg Asp Arg Glu
355             165             170             175
358 Glu Arg Ser Leu Asn Leu Pro Lys Gly Glu Tyr Glu Ile Pro Leu Leu
359             180             185             190
362 Ile Gln Asp Lys Ser Phe His Glu Asp Gly Ser Leu Phe Tyr Pro Arg
363         195             200             205
366 Gln Pro Asp Asn Pro Ser Pro Asp Leu Pro Asp Pro Ser Ile Val Pro
367     210             215             220
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VERIFICATION SUMMARY   DATE: 10/19/2004
PATENT APPLICATION: **US/10/510,408**   TIME: 14:41:01

Input Set : **N:\AMC\PTO.AMC.txt**
Output Set: **N:\CRF4\10192004\J510408.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date